```
                        GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on:          April 27, 2005, 20:16:46 ; Search time 4913 Seconds
                                            (without alignments)
                                            3136.324 Million cell updates/sec

Title:           US-10-616-309-4
Perfect score:   1615
Sequence:        1 MKQLWFAMSLVTGSLLFSAN..........ELPPQTAKRIAENIKFGAAQ 318

Scoring table:   BLOSUM62
                 Xgapop 10.0 , Xgapext  0.5
                 Ygapop 10.0 , Ygapext  0.5
                 Fgapop  6.0 , Fgapext  7.0
                 Delop   6.0 , Delext   7.0

Searched:        4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters:        9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh

Q=/cgn2_1/USPTO_spool/US10616309/runat_26042005_130704_13105/app_query.fasta_1.4
55
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10616309_@CGN_1_1_3731_@runat_26042005_130704_13105 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :       GenEmbl:*
                 1:  gb_ba:*
                 2:  gb_htg:*
                 3:  gb_in:*
                 4:  gb_om:*
                 5:  gb_ov:*
                 6:  gb_pat:*
                 7:  gb_ph:*
                 8:  gb_pl:*
                 9:  gb_pr:*
                 10:  gb_ro:*
```

```
11:  gb_sts:*
12:  gb_sy:*
13:  gb_un:*
14:  gb_vi:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1615	100.0	957	6	CQ759953 App	CQ759953 Sequence
	2	1615	100.0	1661	1	ECU37455 X Dela acnus	U37455 Escherichia
	3	1615	100.0	3192	1	ECU37089 X Raina	U37089 Escherichia
c	4	1615	100.0	10208	1	AE005487 Genome perna	AE005487 Escherich
c	5	1615	100.0	12767	1	AE015278 2002	AE015278 Shigella
c	6	1615	100.0	29254	1	ECOK12RIII	D64044 Escherichia
c	7	1615	100.0	110000	1	U00096_26	Continuation (27 o
c	8	1615	100.0	110000	1	U00096_27	Continuation (28 o
c	9	1615	100.0	270365	1	AP002562 1999 seq	AP002562 Escherich
c	10	1615	100.0	290380	1	AE016987 X	AE016987 Shigella
c	11	1611	99.8	300099	1	AE016764	AE016764 Escherich
	12	1465	90.7	13311	1	STAF001386	AF001386 Salmonell
	13	1465	90.7	13311	6	AX191732	AX191732 Sequence
c	14	1465	90.7	22108	1	AE008819	AE008819 Salmonell
c	15	1461	90.5	145050	1	AL627275	AL627275 Salmonell
	16	1461	90.5	300431	1	AE016835	AE016835 Salmonell
	17	1334	82.6	1041	6	AR387875	AR387875 Sequence
	18	1066	66.0	1122	6	BD248394	BD248394 Gene part
	19	1044	64.6	10886	1	AE013731	AE013731 Yersinia
c	20	1044	64.6	110000	1	BX936398_34	Continuation (35 o
	21	1044	64.6	258050	1	AJ414153	AJ414153 Yersinia
	22	1044	64.6	290294	1	AE017136	AE017136 Yersinia
	23	1041	64.5	4819	1	AY098586	AY098586 Yersinia
c	24	933	57.8	110000	1	BX950851_36	Continuation (37 o
c	25	840	52.0	348505	1	BX571870	BX571870 Photorhab
	26	840	52.0	349980	6	AX770909	AX770909 Sequence
	27	770.5	47.7	3545	1	PHRRPOE	L41667 Photobacter
	28	770.5	47.7	3545	1	PHRRPOEA	L41688 Photobacter
c	29	764.5	47.3	349814	1	CR378673	CR378673 Photobact
	30	749	46.4	1020	6	AR378439	AR378439 Sequence
c	31	739.5	45.8	12162	1	AE004316	AE004316 Vibrio ch
c	32	698.5	43.3	248650	1	AP005341	AP005341 Vibrio vu
	33	698.5	43.3	300732	1	AE016802	AE016802 Vibrio vu
c	34	673	41.7	296650	1	AP005082	AP005082 Vibrio pa
	35	603	37.3	106645	6	CQ873068	CQ873068 Sequence
	36	600	37.2	10631	1	U32746	U32746 Haemophilus
	37	600	37.2	110000	6	BD426631_06	Continuation (7 of
	38	600	37.2	110000	6	AR274513_06	Continuation (7 of
	39	600	37.2	110000	6	AR541453_06	Continuation (7 of
	40	587.5	36.4	110000	1	AE016827_21	Continuation (22 o
c	41	585.5	36.3	11975	1	AE006215	AE006215 Pasteurel
	42	351.5	21.8	10058	1	AE015578	AE015578 Shewanell
	43	336.5	20.8	5000	1	AB189022	AB189022 Shewanell

```
  44   293.5   18.2 301995   1   AE016779        AE016779 Pseudomon
c 45   269.5   16.7   1855    6   CQ872495        CQ872495 Sequence
```

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OM protein - nucleic search, using frame_plus_p2n model

Run on:          April 27, 2005, 20:03:17 ; Search time 610 Seconds
                                           (without alignments)
                                           3086.029 Million cell updates/sec

Title:           US-10-616-309-4
Perfect score:   1615
Sequence:        1 MKQLWFAMSLVTGSLLFSAN.........ELPPQTAKRIAENIKFGAAQ 318

Scoring table:   BLOSUM62
                 Xgapop 10.0 , Xgapext  0.5
                 Ygapop 10.0 , Ygapext  0.5
                 Fgapop  6.0 , Fgapext  7.0
                 Delop   6.0 , Delext   7.0

Searched:        4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters:      8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-
Q=/cgn2_1/USPTO_spool/US10616309/runat_26042005_130704_13093/app_query.fasta_1.4
55
-DB=N_Geneseq_16Dec04 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10616309_@CGN_1_1_470_@runat_26042005_130704_13093 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :       N_Geneseq_16Dec04:*
                 1:  geneseqn1980s:*
                 2:  geneseqn1990s:*
                 3:  geneseqn2000s:*
                 4:  geneseqn2001as:*
                 5:  geneseqn2001bs:*
                 6:  geneseqn2002as:*
                 7:  geneseqn2002bs:*
                 8:  geneseqn2003as:*
                 9:  geneseqn2003bs:*
                 10:  geneseqn2003cs:*
```

```
    11:  geneseqn2003ds:*
    12:  geneseqn2004as:*
    13:  geneseqn2004bs:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1615	100.0	957	12	ADH45224	Adh45224 Enterobac
	2	1334	82.6	1041	11	ACH98809	Ach98809 Klebsiell
	3	1066	66.0	1122	3	AAZ98342	Aaz98342 A. thalia
	4	851	52.7	1968	5	AAS82067	Aas82067 DNA encod
	5	840	52.0	957	10	ACF71993	Acf71993 Photorha
	6	840	52.0	110000	10	ACF67367_51	Continuation (52 o
	7	840	52.0	110000	10	ACF67367_52	Continuation (53 o
	8	840	52.0	110000	10	ACF65387_3	Continuation (4 of
	9	749	46.4	1020	10	ADF03160	Adf03160 Bacterial
	10	603	37.3	106645	13	ADT05645	Adt05645 Haemophil
	11	600	37.2	110000	2	AAT42063_06	Continuation (7 of
c	12	321	19.9	1986	5	AAS92912	Aas92912 DNA encod
c	13	317.5	19.7	2180	5	AAS93271	Aas93271 DNA encod
c	14	269.5	16.7	1855	13	ADT05072	Adt05072 Haemophil
	15	255	15.8	1065	11	ABD14466	Abd14466 Pseudomon
c	16	255	15.8	1308	11	ABD14265	Abd14265 Pseudomon
	17	255	15.8	1800	2	AAQ70238	Aaq70238 P. aerugi
	18	255	15.8	1800	2	AAQ70237	Aaq70237 P. aerugi
	19	255	15.8	1800	3	AAA51920	Aaa51920 P. aerugi
	20	163	10.1	100	8	ACD79772	Acd79772 E. coli K
	21	160	9.9	100	8	ACD79771	Acd79771 E. coli K
	22	157	9.7	100	8	ACD79770	Acd79770 E. coli K
	23	127.5	7.9	342	6	ABN75321	Abn75321 Human ORF
	24	109	6.7	19342	4	AAS59534	Aas59534 Propionib
	25	109	6.7	19342	8	ACF64463	Acf64463 Propionib
	26	104.5	6.5	1635	8	ACA41299	Aca41299 Prokaryot
	27	104.5	6.5	1635	10	ABZ38409	Abz38409 N. gonorr
	28	103	6.4	3459	8	ACA37296	Aca37296 Prokaryot
	29	103	6.4	110000	10	ADF77343_04	Continuation (5 of
	30	101.5	6.3	1170	13	ADS56280	Ads56280 Bacterial
	31	101	6.3	3282	11	ABD06652	Abd06652 Pseudomon
c	32	101	6.3	4158	11	ABD06744	Abd06744 Pseudomon
	33	101	6.3	4953	11	ABD06623	Abd06623 Pseudomon
c	34	100.5	6.2	1374	8	ACA26695	Aca26695 Prokaryot
	35	100.5	6.2	1641	2	AAZ11996	Aaz11996 Neisseria
	36	98	6.1	1995	8	ACA23302	Aca23302 Prokaryot
	37	96	5.9	1494	11	ABD16357	Abd16357 Pseudomon
c	38	96	5.9	1509	11	ABD16065	Abd16065 Pseudomon
	39	96	5.9	15272	4	ABL03697	Abl03697 Drosophil
	40	95.5	5.9	1221	6	ABN68595	Abn68595 Streptoco
	41	95.5	5.9	1224	8	ACA50778	Aca50778 Prokaryot
	42	95	5.9	14391	13	ADS96571	Ads96571 Drosophil
	43	95	5.9	46593	3	AAA81456	Aaa81456 N. mening
	44	95	5.9	110000	3	AAA81489_5	Continuation (6 of

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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 27, 2005, 23:02:11 ; Search time 203 Seconds
                                           (without alignments)
                                           2563.232 Million cell updates/sec

Title: US-10-616-309-4
Perfect score: 1615
Sequence: 1 MKQLWFAMSLVTGSLLFSAN..........ELPPQTAKRIAENIKFGAAQ 318

Scoring table: BLOSUM62
                 Xgapop 10.0 , Xgapext 0.5
                 Ygapop 10.0 , Ygapext 0.5
                 Fgapop 6.0 , Fgapext 7.0
                 Delop   6.0 , Delext   7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-
Q=/cgn2_1/USPTO_spool/US10616309/runat_26042005_130705_13155/app_query.fasta_1.4
55
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10616309_@CGN_1_1_69_@runat_26042005_130705_13155 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   Issued_Patents_NA:*
                 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
                 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
                 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
                 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
                 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description	
	1	1334	82.6	1041	4	US-09-489-039A-4604 X	Sequence 4604, Ap	*Diagnostics Therapeutics*
	2	749	46.4	1020	4	US-09-543-681A-3445 X	Sequence 3445, Ap	
	3	600	37.2	1830121	4	US-09-557-884-1 *Itac*	Sequence 1, Appli	
	4	600	37.2	1830121	4	US-09-643-990A-1 *HGS*	Sequence 1, Appli	
	5	255	15.8	1065	4	US-09-252-991A-13070	Sequence 13070, A	
c	6	255	15.8	1308	4	US-09-252-991A-12869	Sequence 12869, A	
	7	255	15.8	1800	1	US-08-260-202A-10	Sequence 10, Appl	
	8	255	15.8	1800	1	US-08-017-114-10	Sequence 10, Appl	
	9	255	15.8	1800	3	US-08-505-307-10	Sequence 10, Appl	
	10	255	15.8	1800	3	US-09-609-151A-10	Sequence 10, Appl	
	11	255	15.8	1800	5	PCT-US94-02034-10	Sequence 10, Appl	
	12	102.5	6.3	2112	4	US-09-902-540-3277	Sequence 3277, Ap	
c	13	102.5	6.3	17480	4	US-09-902-540-1151	Sequence 1151, Ap	
	14	101	6.3	3282	4	US-09-252-991A-5256	Sequence 5256, Ap	
c	15	101	6.3	4158	4	US-09-252-991A-5348	Sequence 5348, Ap	
	16	101	6.3	4953	4	US-09-252-991A-5227	Sequence 5227, Ap	
	17	96	5.9	1494	4	US-09-252-991A-14961	Sequence 14961, A	
c	18	96	5.9	1509	4	US-09-252-991A-14669	Sequence 14669, A	
	19	93.5	5.8	16423	4	US-09-902-540-1120	Sequence 1120, Ap	
c	20	93	5.8	11563	4	US-09-902-540-1019	Sequence 1019, Ap	
	21	93	5.8	246444	4	US-09-949-016-13113	Sequence 13113, A	
	22	92	5.7	2256	4	US-09-902-540-6853	Sequence 6853, Ap	
c	23	92	5.7	4302	4	US-09-902-540-576	Sequence 576, App	
c	24	92	5.7	9146	4	US-09-902-540-990	Sequence 990, App	
	25	91	5.6	1830	4	US-09-252-991A-3563	Sequence 3563, Ap	
c	26	91	5.6	1926	4	US-09-252-991A-3531	Sequence 3531, Ap	
	27	90.5	5.6	830	4	US-09-593-887-5	Sequence 5, Appli	
	28	90	5.6	1668	4	US-09-252-991A-15085	Sequence 15085, A	
	29	90	5.6	3288	4	US-09-107-532A-201	Sequence 201, App	
	30	90	5.6	11647	4	US-09-949-016-12059	Sequence 12059, A	
	31	90	5.6	11648	4	US-09-949-016-13801	Sequence 13801, A	
	32	89.5	5.5	2172	1	US-07-982-712-1	Sequence 1, Appli	
	33	89.5	5.5	536165	4	US-09-214-808-1	Sequence 1, Appli	
	34	89	5.5	1245	3	US-09-242-050-1	Sequence 1, Appli	
	35	89	5.5	2036	4	US-09-949-016-2059	Sequence 2059, Ap	
	36	88.5	5.5	1575	4	US-09-252-991A-3100	Sequence 3100, Ap	
c	37	88.5	5.5	4859	3	US-09-453-702B-154	Sequence 154, App	
c	38	88.5	5.5	5536	4	US-09-902-540-803	Sequence 803, App	
	39	88	5.4	1530	4	US-09-252-991A-13672	Sequence 13672, A	
	40	88	5.4	1815	4	US-09-252-991A-7621	Sequence 7621, Ap	
c	41	88	5.4	1932	4	US-09-252-991A-7931	Sequence 7931, Ap	
	42	88	5.4	2925	4	US-09-252-991A-7069	Sequence 7069, Ap	
c	43	88	5.4	4185	3	US-08-961-527-173	Sequence 173, App	
	44	88	5.4	5523	4	US-09-902-540-3952	Sequence 3952, Ap	
c	45	88	5.4	5658	4	US-09-647-344A-17	Sequence 17, Appl	

```
Db      1188 GAGGTCGCCGCGGGCGTTGCGCCGCTCGTCC------------GGCTCGACGCCGGCTTC 1141

Qy       272 rThrAspGlnMetLeuArgThrGlyArgArgThrValSerThrSerValArgAspAsnAl 292
             |  ·         |||       ||||||      |||::::::::::|||     ||
Db      1140 GATCACCCCGGCGTTG------TCGAGGCGCGCGGCGTCCAGCGCGATGCGTTCGCGCGC 1087

Qy       292 a----------------------GluIleThrIleValGlyGluLeuProPro 302
             |                                :::      |||||||||
Db      1086 CGCCAGGCTCTGCCGGTTGACCAGTTCCTCCGCGCTGCGGATCTCGGCGCTGCCACCG 1029
```

Search completed: April 28, 2005, 03:01:07
Job time : 834 secs

                          GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 27, 2005, 23:14:21 ; Search time 648 Seconds
                                             (without alignments)
                                             2979.312 Million cell updates/sec

Title: US-10-616-309-4
Perfect score: 1615
Sequence: 1 MKQLWFAMSLVTGSLLFSAN.........ELPPQTAKRIAENIKFGAAQ 318

Scoring table: BLOSUM62
                   Xgapop 10.0 , Xgapext 0.5
                   Ygapop 10.0 , Ygapext 0.5
                   Fgapop 6.0 , Fgapext 7.0
                   Delop   6.0 , Delext   7.0

Searched: 5633728 seqs, 3035525691 residues

Total number of hits satisfying chosen parameters: 11267456

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-
Q=/cgn2_1/USPTO_spool/US10616309/runat_26042005_130705_13131/app_query.fasta_1.4
55
-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10616309_@CGN_1_1_480_@runat_26042005_130705_13131
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
```

-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :        Published_Applications_NA:*
                  1:  /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
                  2:  /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
                  3:  /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
                  4:  /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
                  5:  /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
                  6:  /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
                  7:  /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
                  8:  /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
                  9:  /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
                  10:  /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
                  11:  /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
                  12:  /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
                  13:  /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
                  14:  /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
                  15:  /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
                  16:  /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
                  17:  /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
                  18:  /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
                  19:  /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
                  20:  /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
                  21:  /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
                  22:  /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

              %
Result        Query
   No.  Score  Match  Length  DB  ID                            Description
------------------------------------------------------------------------------
    1   1615  100.0     957   19  US-10-616-309-3  *Appl*        Sequence 3, Appli *plant*
    2   1066   66.0    1122   16  US-10-342-224-75 *X*           Sequence 75, Appl
    3    600   37.2 1830121   17  US-10-329-670-1  *Hal*         Sequence 1, Appli
    4    600   37.2 1830121   18  US-10-158-865-1  *//*          Sequence 1, Appli
    5  127.5    7.9     342   11  US-09-864-408A-535            Sequence 535, App
    6    106    6.6     855   15  US-10-156-761-4327            Sequence 4327, Ap
c   7    106    6.6 9025608   15  US-10-156-761-1               Sequence 1, Appli
    8    105    6.5    1745   18  US-10-767-701-13257           Sequence 13257, A
    9  104.5    6.5    1635   17  US-10-282-122A-29169          Sequence 29169, A
   10    103    6.4    3459   17  US-10-282-122A-25166          Sequence 25166, A
c  11  102.5    6.3    2603   18  US-10-425-115-58128           Sequence 58128, A
   12  101.5    6.3    1170   17  US-10-369-493-31954           Sequence 31954, A
c  13  100.5    6.2    1374   17  US-10-282-122A-14565          Sequence 14565, A
   14   98.5    6.1    2357   17  US-10-424-599-19556           Sequence 19556, A
   15     98    6.1    1995   17  US-10-282-122A-11172          Sequence 11172, A
   16   97.5    6.0 9025608   15  US-10-156-761-1               Sequence 1, Appli
   17     96    5.9    1275   18  US-10-437-963-62362           Sequence 62362, A
   18   95.5    5.9     637   17  US-10-424-599-75055           Sequence 75055, A
   19   95.5    5.9    1224   17  US-10-282-122A-38648          Sequence 38648, A
   20   95.5    5.9    1224   18  US-10-474-792-119             Sequence 119, App
   21   95.5    5.9    3066   15  US-10-156-761-1742            Sequence 1742, Ap
   22   95.5    5.9    3511   18  US-10-437-963-51948           Sequence 51948, A

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on:          April 27, 2005, 20:23:46 ; Search time 3680 Seconds
                                            (without alignments)
                                            3289.249 Million cell updates/sec

Title:           US-10-616-309-4
Perfect score:   1615
Sequence:        1 MKQLWFAMSLVTGSLLFSAN..........ELPPQTAKRIAENIKFGAAQ 318

Scoring table:   BLOSUM62
                 Xgapop 10.0 , Xgapext  0.5
                 Ygapop 10.0 , Ygapext  0.5
                 Fgapop  6.0 , Fgapext  7.0
                 Delop   6.0 , Delext   7.0

Searched:        34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters:      68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-
Q=/cgn2_1/USPTO_spool/US10616309/runat_26042005_130705_13115/app_query.fasta_1.4
55
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10616309_@CGN_1_1_3437_@runat_26042005_130705_13115 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :       EST:*
                 1:  gb_est1:*
                 2:  gb_est2:*
                 3:  gb_htc:*
                 4:  gb_est3:*
                 5:  gb_est4:*
                 6:  gb_est5:*
                 7:  gb_est6:*
                 8:  gb_gss1:*
                 9:  gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|---|
| c | 1 | 335 | 20.7 | 535 | 9 | CL667196 | CL667196 PRI0154b_ |
|   | 2 | 316 | 19.6 | 798 | 9 | CL679590 | CL679590 PRI0126c_ |
| c | 3 | 315.5 | 19.5 | 552 | 8 | AQ990079 | AQ990079 Rfc00790 |
|   | 4 | 119 | 7.4 | 650 | 8 | BZ367313 | BZ367313 id03f12.b |
|   | 5 | 110 | 6.8 | 828 | 8 | BZ559729 | BZ559729 pacs2-164 |
| c | 6 | 98.5 | 6.1 | 794 | 9 | CG448483 | CG448483 OGTCB40TV |
| c | 7 | 98 | 6.1 | 711 | 9 | CL860410 | CL860410 OR_CBa009 |
|   | 8 | 98 | 6.1 | 2095 | 3 | CNS0A1PU | BX830564 Arabidops |
|   | 9 | 97.5 | 6.0 | 1857 | 3 | AK080782 | AK080782 Mus muscu |
|   | 10 | 97.5 | 6.0 | 3830 | 3 | AK031181 | AK031181 Mus muscu |
|   | 11 | 97 | 6.0 | 890 | 5 | BU188866 | BU188866 AGENCOURT |
| c | 12 | 97 | 6.0 | 1068 | 4 | BG423398 | BG423398 602449239 |
|   | 13 | 97 | 6.0 | 1149 | 4 | BG246201 | BG246201 602359102 |
|   | 14 | 96.5 | 6.0 | 380 | 7 | CN252855 | CN252855 EST018791 |
|   | 15 | 96.5 | 6.0 | 560 | 7 | CN250672 | CN250672 EST016597 |
|   | 16 | 96.5 | 6.0 | 782 | 6 | CD576521 | CD576521 UCRPT01_0 |
|   | 17 | 96.5 | 6.0 | 871 | 6 | CD574232 | CD574232 UCRPT01_0 |
|   | 18 | 96 | 5.9 | 3386 | 3 | AK046666 | AK046666 Mus muscu |
|   | 19 | 95.5 | 5.9 | 612 | 7 | CN244788 | CN244788 EST010667 |
|   | 20 | 95 | 5.9 | 800 | 8 | BZ401449 | BZ401449 EINDF04TF |
| c | 21 | 95 | 5.9 | 838 | 8 | BZ391409 | BZ391409 EINBH65TR |
|   | 22 | 94 | 5.8 | 515 | 6 | CA375958 | CA375958 654186 NC |
| c | 23 | 93.5 | 5.8 | 493 | 2 | BF651566 | BF651566 274381 MA |
|   | 24 | 93.5 | 5.8 | 516 | 6 | CB065020 | CB065020 px86h04.y |
|   | 25 | 93 | 5.8 | 682 | 4 | BJ235699 | BJ235699 BJ235699 |
| c | 26 | 93 | 5.8 | 703 | 9 | CE102856 | CE102856 tigr-gss- |
|   | 27 | 93 | 5.8 | 737 | 7 | CK656702 | CK656702 3017HAEMU |
|   | 28 | 92.5 | 5.7 | 763 | 5 | BX090614 | BX090614 BX090614 |
| c | 29 | 92.5 | 5.7 | 822 | 3 | CNS08PKF | BX022555 Single re |
|   | 30 | 92.5 | 5.7 | 853 | 6 | CA280028 | CA280028 SCVPLB2C0 |
|   | 31 | 92 | 5.7 | 595 | 9 | CE127506 | CE127506 tigr-gss- |
|   | 32 | 92 | 5.7 | 616 | 6 | CD082980 | CD082980 MA3-9999U |
| c | 33 | 92 | 5.7 | 633 | 7 | CN911036 | CN911036 021119ABM |
|   | 34 | 92 | 5.7 | 664 | 6 | CD082227 | CD082227 MA3-9999U |
|   | 35 | 92 | 5.7 | 704 | 6 | CD079868 | CD079868 MA3-9999U |
|   | 36 | 92 | 5.7 | 722 | 6 | CD835383 | CD835383 BN45.045F |
| c | 37 | 92 | 5.7 | 861 | 6 | CB316085 | CB316085 AGENCOURT |
| c | 38 | 92 | 5.7 | 976 | 5 | BU849602 | BU849602 AGENCOURT |
|   | 39 | 92 | 5.7 | 988 | 5 | BQ961211 | BQ961211 AGENCOURT |
|   | 40 | 92 | 5.7 | 1788 | 9 | CL973619 | CL973619 OsIFCC024 |
| c | 41 | 91.5 | 5.7 | 632 | 4 | BJ799561 | BJ799561 BJ799561 |
| c | 42 | 91.5 | 5.7 | 869 | 4 | BI660875 | BI660875 603303929 |
|   | 43 | 91.5 | 5.7 | 1506 | 3 | AK078318 | AK078318 Mus muscu |
| c | 44 | 91 | 5.6 | 685 | 7 | CK976531 | CK976531 4108010 B |
| c | 45 | 91 | 5.6 | 689 | 7 | CK977911 | CK977911 4109407 B |

ALIGNMENTS